

## SEQUENCE LISTING

<110> Buchter-Larsen, et al.

<120> A PROCESS OF PREPARING AN ANTI-OXIDANT

<130> 674509-2020

<140> 09/423,126

<141> 1999-11-05

<150> PCT/IB98/00708

<151> 1998-05-06

<150> GB 9709161.5

<151> 1997-05-06

<160> 12

<170> PatentIn version 3.0

<210> 1

<211> 1088

<212> PRT

<213> Unknown

<220>

<223> fungus sp. or fungus infected gracilariopsis sp.

<400> 1

Met Phe Ser Thr Leu Ala Phe Val Ala Pro Ser Ala Leu Gly Ala Ser  
1 5 10 15

Thr Phe Val Gly Ala Glu Val Arg Ser Asn Val Arg Ile His Ser Ala  
20 25 30

Phe Pro Ala Val His Thr Ala Thr Arg Lys Thr Asn Arg Leu Asn Val  
35 40 45

Ser Met Thr Ala Leu Ser Asp Lys Gln Thr Ala Thr Ala Gly Ser Thr  
50 55 60

Asp Asn Pro Asp Gly Ile Asp Tyr Lys Thr Tyr Asp Tyr Val Gly Val  
65 70 75 80

Trp Gly Phe Ser Pro Leu Ser Asn Thr Asn Trp Phe Ala Ala Gly Ser  
85 90 95

Ser Thr Pro Gly Gly Ile Thr Asp Trp Thr Ala Thr Met Asn Val Asn  
100 105 110

Phe Asp Arg Ile Asp Asn Pro Ser Ile Thr Val Gln His Pro Val Gln  
115 120 125

Val Gln Val Thr Ser Tyr Asn Asn Asn Ser Tyr Arg Val Arg Phe Asn  
130 135 140

Pro Asp Gly Pro Ile Arg Asp Val Thr Arg Gly Pro Ile Leu Lys Gln															
145				150					155						160
Gln Leu Asp Trp Ile Arg Thr Gln Glu Leu Ser Glu Gly Cys Asp Pro				165					170					175	
Gly Met Thr Phe Thr Ser Glu Gly Phe Leu Thr Phe Glu Thr Lys Asp				180					185					190	
Leu Ser Val Ile Ile Tyr Gly Asn Phe Lys Thr Arg Val Thr Arg Lys				195					200					205	
Ser Asp Gly Lys Val Ile Met Glu Asn Asp Glu Val Gly Thr Ala Ser				210					215					220	
Ser Gly Asn Lys Cys Arg Gly Leu Met Phe Val Asp Arg Leu Tyr Gly				225					230					235	240
Asn Ala Ile Ala Ser Val Asn Lys Asn Phe Arg Asn Asp Ala Val Lys				245					250					255	
Gln Glu Gly Phe Tyr Gly Ala Gly Glu Val Asn Cys Lys Tyr Gln Asp				260					265					270	
Thr Tyr Ile Leu Glu Arg Thr Gly Ile Ala Met Thr Asn Tyr Asn Tyr				275					280					285	
Asp Asn Leu Asn Tyr Asn Gln Trp Asp Leu Arg Pro Pro His His Asp				290					295					300	
Gly Ala Leu Asn Pro Asp Tyr Tyr Ile Pro Met Tyr Tyr Ala Ala Pro				305					310					315	320
Trp Leu Ile Val Asn Gly Cys Ala Gly Thr Ser Glu Gln Tyr Ser Tyr				325					330					335	
Gly Trp Phe Met Asp Asn Val Ser Gln Ser Tyr Met Asn Thr Gly Asp				340					345					350	
Thr Thr Trp Asn Ser Gly Gln Glu Asp Leu Ala Tyr Met Gly Ala Gln				355					360					365	
Tyr Gly Pro Phe Asp Gln His Phe Val Tyr Gly Ala Gly Gly Gly Met				370					375					380	
Glu Cys Val Val Thr Ala Phe Ser Leu Leu Gln Gly Lys Glu Phe Glu				385					390					395	400
Asn Gln Val Leu Asn Lys Arg Ser Val Met Pro Pro Lys Tyr Val Phe				405					410					415	
Gly Phe Phe Gln Gly Val Phe Gly Thr Ser Ser Leu Leu Arg Ala His				420					425					430	
Met Pro Ala Gly Glu Asn Asn Ile Ser Val Glu Glu Ile Val Glu Gly				435					440					445	

Tyr	Gln	Asn	Asn	Asn	Phe	Pro	Phe	Glu	Gly	Leu	Ala	Val	Asp	Val	Asp		
450						455					460						
Met	Gln	Asp	Asn	Leu	Arg	Val	Phe	Thr	Thr	Lys	Gly	Glu	Phe	Trp	Thr		
465					470					475					480		
Ala	Asn	Arg	Val	Gly	Thr	Gly	Gly	Asp	Pro	Asn	Asn	Arg	Ser	Val	Phe		
				485					490					495			
Glu	Trp	Ala	His	Asp	Lys	Gly	Leu	Val	Cys	Gln	Thr	Asn	Ile	Thr	Cys		
			500					505					510				
Phe	Leu	Arg	Asn	Asp	Asn	Glu	Gly	Gln	Asp	Tyr	Glu	Val	Asn	Gln	Thr		
		515					520					525					
Leu	Arg	Glu	Arg	Gln	Leu	Tyr	Thr	Lys	Asn	Asp	Ser	Leu	Thr	Gly	Thr		
		530				535					540						
Asp	Phe	Gly	Met	Thr	Asp	Asp	Gly	Pro	Ser	Asp	Ala	Tyr	Ile	Gly	His		
545					550					555					560		
Leu	Asp	Tyr	Gly	Gly	Gly	Val	Glu	Cys	Asp	Ala	Leu	Phe	Pro	Asp	Trp		
			565						570					575			
Gly	Arg	Pro	Asp	Val	Ala	Glu	Trp	Trp	Gly	Asn	Asn	Tyr	Lys	Lys	Leu		
			580					585					590				
Phe	Ser	Ile	Gly	Leu	Asp	Phe	Val	Trp	Gln	Asp	Met	Thr	Val	Pro	Ala		
		595					600					605					
Met	Met	Pro	His	Lys	Ile	Gly	Asp	Asp	Ile	Asn	Val	Lys	Pro	Asp	Gly		
610						615					620						
Asn	Trp	Pro	Asn	Ala	Asp	Asp	Pro	Ser	Asn	Gly	Gln	Tyr	Asn	Trp	Lys		
625				630						635					640		
Thr	Tyr	His	Pro	Gln	Val	Leu	Val	Thr	Asp	Met	Arg	Tyr	Glu	Asn	His		
				645					650					655			
Gly	Arg	Glu	Pro	Met	Val	Thr	Gln	Arg	Asn	Ile	His	Ala	Tyr	Thr	Leu		
			660					665					670				
Cys	Glu	Ser	Thr	Arg	Lys	Glu	Gly	Ile	Val	Glu	Asn	Ala	Asp	Thr	Leu		
		675					680					685					
Thr	Lys	Phe	Arg	Arg	Ser	Tyr	Ile	Ile	Ser	Arg	Gly	Gly	Tyr	Ile	Gly		
690					695						700						
Asn	Gln	His	Phe	Gly	Gly	Met	Trp	Val	Gly	Asp	Asn	Ser	Thr	Thr	Ser		
705					710					715					720		
Asn	Tyr	Ile	Gln	Met	Met	Ile	Ala	Asn	Asn	Ile	Asn	Met	Asn	Met	Ser		
				725					730					735			
Cys	Leu	Pro	Leu	Val	Gly	Ser	Asp	Ile	Gly	Gly	Phe	Thr	Ser	Tyr	Asp		
			740					745					750				

Asn Glu Asn Gln Arg Thr Pro Cys Thr Gly Asp Leu Met Val Arg Tyr  
 755 760 765  
 Val Gln Ala Gly Cys Leu Leu Pro Trp Phe Arg Asn His Tyr Asp Arg  
 770 775 780  
 Trp Ile Glu Ser Lys Asp His Gly Lys Asp Tyr Gln Glu Leu Tyr Met  
 785 790 795 800  
 Tyr Pro Asn Glu Met Asp Thr Leu Arg Lys Phe Val Glu Phe Arg Tyr  
 805 810 815  
 Arg Trp Gln Glu Val Leu Tyr Thr Ala Met Tyr Gln Asn Ala Ala Phe  
 820 825 830  
 Gly Lys Pro Ile Ile Lys Ala Ala Ser Met Tyr Asn Asn Asp Ser Asn  
 835 840 845  
 Val Arg Arg Ala Gln Asn Asp His Phe Leu Leu Gly Gly His Asp Gly  
 850 855 860  
 Tyr Arg Ile Leu Cys Ala Pro Val Val Trp Glu Asn Ser Thr Glu Arg  
 865 870 875 880  
 Glu Leu Tyr Leu Pro Val Leu Thr Gln Trp Tyr Lys Phe Gly Pro Asp  
 885 890 895  
 Phe Asp Thr Lys Pro Leu Glu Gly Ala Met Asn Gly Gly Asp Arg Ile  
 900 905 910  
 Tyr Asn Tyr Pro Val Pro Gln Ser Glu Ser Pro Ile Phe Val Arg Glu  
 915 920 925  
 Gly Ala Ile Leu Pro Thr Arg Tyr Thr Leu Asn Gly Glu Asn Lys Ser  
 930 935 940  
 Leu Asn Thr Tyr Thr Asp Glu Asp Pro Leu Val Phe Glu Val Phe Pro  
 945 950 955 960  
 Leu Gly Asn Asn Arg Ala Asp Gly Met Cys Tyr Leu Asp Asp Gly Gly  
 965 970 975  
 Val Thr Thr Asn Ala Glu Asp Asn Gly Lys Phe Ser Val Val Lys Val  
 980 985 990  
 Ala Ala Glu Gln Asp Gly Gly Thr Glu Thr Ile Thr Phe Thr Asn Asp  
 995 1000 1005  
 Cys Tyr Glu Tyr Val Phe Gly Gly Pro Phe Tyr Val Arg Val Arg  
 1010 1015 1020  
 Gly Ala Gln Ser Pro Ser Asn Ile His Val Ser Ser Gly Ala Gly  
 1025 1030 1035  
 Ser Gln Asp Met Lys Val Ser Ser Ala Thr Ser Arg Ala Ala Leu  
 1040 1045 1050

Phe Asn Asp Gly Glu Asn Gly Asp Phe Trp Val Asp Gln Glu Thr  
 1055 1060 1065

Asp Ser Leu Trp Leu Lys Leu Pro Asn Val Val Leu Pro Asp Ala  
 1070 1075 1080

Val Ile Thr Ile Thr  
 1085

<210> 2  
 <211> 1091  
 <212> PRT  
 <213> Unknown

<220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.

<400> 2

Met Tyr Pro Thr Leu Thr Phe Val Ala Pro Ser Ala Leu Gly Ala Arg  
 1 5 10 15

Thr Phe Thr Cys Val Gly Ile Phe Arg Ser His Ile Leu Ile His Ser  
 20 25 30

Val Val Pro Ala Val Arg Leu Ala Val Arg Lys Ser Asn Arg Leu Asn  
 35 40 45

Val Ser Met Ser Ala Leu Phe Asp Lys Pro Thr Ala Val Thr Gly Gly  
 50 55 60

Lys Asp Asn Pro Asp Asn Ile Asn Tyr Thr Thr Tyr Asp Tyr Val Pro  
 65 70 75 80

Val Trp Arg Phe Asp Pro Leu Ser Asn Thr Asn Trp Phe Ala Ala Gly  
 85 90 95

Ser Ser Thr Pro Gly Asp Ile Asp Asp Trp Thr Ala Thr Met Asn Val  
 100 105 110

Asn Phe Asp Arg Ile Asp Asn Pro Ser Phe Thr Leu Glu Lys Pro Val  
 115 120 125

Gln Val Gln Val Thr Ser Tyr Lys Asn Asn Cys Phe Arg Val Arg Phe  
 130 135 140

Asn Pro Asp Gly Pro Ile Arg Asp Val Asp Arg Gly Pro Ile Leu Gln  
 145 150 155 160

Gln Gln Leu Asn Trp Ile Arg Lys Gln Glu Gln Ser Lys Gly Phe Asp  
 165 170 175

Pro Lys Met Gly Phe Thr Lys Glu Gly Phe Leu Lys Phe Glu Thr Lys  
 180 185 190

Asp Leu Asn Val Ile Ile Tyr Gly Asn Phe Lys Thr Arg Val Thr Arg

195					200					205					
Lys	Arg	Asp	Gly	Lys	Gly	Ile	Met	Glu	Asn	Asn	Glu	Val	Pro	Ala	Gly
210						215					220				
Ser	Leu	Gly	Asn	Lys	Cys	Arg	Gly	Leu	Met	Phe	Val	Asp	Arg	Leu	Tyr
225					230					235					240
Gly	Thr	Ala	Ile	Ala	Ser	Val	Asn	Glu	Asn	Tyr	Arg	Asn	Asp	Pro	Asp
				245					250					255	
Arg	Lys	Glu	Gly	Phe	Tyr	Gly	Ala	Gly	Glu	Val	Asn	Cys	Glu	Phe	Trp
			260					265					270		
Asp	Ser	Glu	Gln	Asn	Arg	Asn	Lys	Tyr	Ile	Leu	Glu	Arg	Thr	Gly	Ile
		275					280					285			
Ala	Met	Thr	Asn	Tyr	Asn	Tyr	Asp	Asn	Tyr	Asn	Tyr	Asn	Gln	Ser	Asp
	290					295					300				
Leu	Ile	Ala	Pro	Gly	Tyr	Pro	Ser	Asp	Pro	Asn	Phe	Tyr	Ile	Pro	Met
305					310					315					320
Tyr	Phe	Ala	Ala	Pro	Trp	Val	Val	Val	Lys	Gly	Cys	Ser	Gly	Asn	Ser
				325					330					335	
Asp	Glu	Gln	Tyr	Ser	Tyr	Gly	Trp	Phe	Met	Asp	Asn	Val	Ser	Gln	Thr
			340					345					350		
Tyr	Met	Asn	Thr	Gly	Gly	Thr	Ser	Trp	Asn	Cys	Gly	Glu	Glu	Asn	Leu
		355					360					365			
Ala	Tyr	Met	Gly	Ala	Gln	Cys	Gly	Pro	Phe	Asp	Gln	His	Phe	Val	Tyr
	370					375					380				
Gly	Asp	Gly	Asp	Gly	Leu	Glu	Asp	Val	Val	Gln	Ala	Phe	Ser	Leu	Leu
385					390					395					400
Gln	Gly	Lys	Glu	Phe	Glu	Asn	Gln	Val	Leu	Asn	Lys	Arg	Ala	Val	Met
			405						410					415	
Pro	Pro	Lys	Tyr	Val	Phe	Gly	Tyr	Phe	Gln	Gly	Val	Phe	Gly	Ile	Ala
			420				425					430			
Ser	Leu	Leu	Arg	Glu	Gln	Arg	Pro	Glu	Gly	Gly	Asn	Asn	Ile	Ser	Val
		435					440					445			
Gln	Glu	Ile	Val	Glu	Gly	Tyr	Gln	Ser	Asn	Asn	Phe	Pro	Leu	Glu	Gly
	450					455					460				
Leu	Ala	Val	Asp	Val	Asp	Met	Gln	Gln	Asp	Leu	Arg	Val	Phe	Thr	Thr
465					470					475					480
Lys	Ile	Glu	Phe	Trp	Thr	Ala	Asn	Lys	Val	Gly	Thr	Gly	Gly	Asp	Ser
			485					490						495	
Asn	Asn	Lys	Ser	Val	Phe	Glu	Trp	Ala	His	Asp	Lys	Gly	Leu	Val	Cys

500					505					510					
Gln	Thr	Asn	Val	Thr	Cys	Phe	Leu	Arg	Asn	Asp	Asn	Gly	Gly	Ala	Asp
		515					520					525			
Tyr	Glu	Val	Asn	Gln	Thr	Leu	Arg	Glu	Lys	Gly	Leu	Tyr	Thr	Lys	Asn
		530					535					540			
Asp	Ser	Leu	Thr	Asn	Thr	Asn	Phe	Gly	Thr	Thr	Asn	Asp	Gly	Pro	Ser
		545					550					555			
Asp	Ala	Tyr	Ile	Gly	His	Leu	Asp	Tyr	Gly	Gly	Gly	Gly	Asn	Cys	Asp
				565					570					575	
Ala	Leu	Phe	Pro	Asp	Trp	Gly	Arg	Pro	Gly	Val	Ala	Glu	Trp	Trp	Gly
				580					585					590	
Asp	Asn	Tyr	Ser	Lys	Leu	Phe	Lys	Ile	Gly	Leu	Asp	Phe	Val	Trp	Gln
		595					600					605			
Asp	Met	Thr	Val	Pro	Ala	Met	Met	Pro	His	Lys	Val	Gly	Asp	Ala	Val
		610					615					620			
Asp	Thr	Arg	Ser	Pro	Tyr	Gly	Trp	Pro	Asn	Glu	Asn	Asp	Pro	Ser	Asn
		625					630					635			
Gly	Arg	Tyr	Asn	Trp	Lys	Ser	Tyr	His	Pro	Gln	Val	Leu	Val	Thr	Asp
				645					650					655	
Met	Arg	Tyr	Glu	Asn	His	Gly	Arg	Glu	Pro	Met	Phe	Thr	Gln	Arg	Asn
			660					665					670		
Met	His	Ala	Tyr	Thr	Leu	Cys	Glu	Ser	Thr	Arg	Lys	Glu	Gly	Ile	Val
			675				680					685			
Ala	Asn	Ala	Asp	Thr	Leu	Thr	Lys	Phe	Arg	Arg	Ser	Tyr	Ile	Ile	Ser
			690				695					700			
Arg	Gly	Gly	Tyr	Ile	Gly	Asn	Gln	His	Phe	Gly	Gly	Met	Trp	Val	Gly
			705				710					715			
Asp	Asn	Ser	Ser	Ser	Gln	Arg	Tyr	Leu	Gln	Met	Met	Ile	Ala	Asn	Ile
				725					730					735	
Val	Asn	Met	Asn	Met	Ser	Cys	Leu	Pro	Leu	Val	Gly	Ser	Asp	Ile	Gly
				740					745					750	
Gly	Phe	Thr	Ser	Tyr	Asp	Gly	Arg	Asn	Val	Cys	Pro	Gly	Asp	Leu	Met
			755				760					765			
Val	Arg	Phe	Val	Gln	Ala	Gly	Cys	Leu	Leu	Pro	Trp	Phe	Arg	Asn	His
			770				775					780			
Tyr	Gly	Arg	Leu	Val	Glu	Gly	Lys	Gln	Glu	Gly	Lys	Tyr	Tyr	Gln	Glu
			785				790					795			
Leu	Tyr	Met	Tyr	Lys	Asp	Glu	Met	Ala	Thr	Leu	Arg	Lys	Phe	Ile	Glu

805										810					815				
Phe	Arg	Tyr	Arg	Trp	Gln	Glu	Val	Leu	Tyr	Thr	Ala	Met	Tyr	Gln	Asn				
			820					825					830						
Ala	Ala	Phe	Gly	Lys	Pro	Ile	Ile	Lys	Ala	Ala	Ser	Met	Tyr	Asp	Asn				
		835				840						845							
Asp	Arg	Asn	Val	Arg	Gly	Ala	Gln	Asp	Asp	His	Phe	Leu	Leu	Gly	Gly				
		850				855					860								
His	Asp	Gly	Tyr	Arg	Ile	Leu	Cys	Ala	Pro	Val	Val	Trp	Glu	Asn	Thr				
		865			870						875				880				
Thr	Ser	Arg	Asp	Leu	Tyr	Leu	Pro	Val	Leu	Thr	Lys	Trp	Tyr	Lys	Phe				
			885						890					895					
Gly	Pro	Asp	Tyr	Asp	Thr	Lys	Arg	Leu	Asp	Ser	Ala	Leu	Asp	Gly	Gly				
			900					905					910						
Gln	Met	Ile	Lys	Asn	Tyr	Ser	Val	Pro	Gln	Ser	Asp	Ser	Pro	Ile	Phe				
		915					920					925							
Val	Arg	Glu	Gly	Ala	Ile	Leu	Pro	Thr	Arg	Tyr	Thr	Leu	Asp	Gly	Ser				
		930				935					940								
Asn	Lys	Ser	Met	Asn	Thr	Tyr	Thr	Asp	Lys	Asp	Pro	Leu	Val	Phe	Glu				
					950				955						960				
Val	Phe	Pro	Leu	Gly	Asn	Asn	Arg	Ala	Asp	Gly	Met	Cys	Tyr	Leu	Asp				
			965					970					975						
Asp	Gly	Gly	Ile	Thr	Thr	Asp	Ala	Glu	Asp	His	Gly	Lys	Phe	Ser	Val				
			980					985					990						
Ile	Asn	Val	Glu	Ala	Leu	Arg	Lys	Gly	Val	Thr	Thr	Thr	Ile	Lys	Phe				
		995					1000						1005						
Ala	Tyr	Asp	Thr	Tyr	Gln	Tyr	Val	Phe	Asp	Gly	Pro	Phe	Tyr	Val					
		1010				1015					1020								
Arg	Ile	Arg	Asn	Leu	Thr	Thr	Ala	Ser	Lys	Ile	Asn	Val	Ser	Ser					
		1025				1030					1035								
Gly	Ala	Gly	Glu	Glu	Asp	Met	Thr	Pro	Thr	Ser	Ala	Asn	Ser	Arg					
		1040				1045					1050								
Ala	Ala	Leu	Phe	Ser	Asp	Gly	Gly	Val	Gly	Glu	Tyr	Trp	Ala	Asp					
		1055				1060					1065								
Asn	Asp	Thr	Ser	Ser	Leu	Trp	Met	Lys	Leu	Pro	Asn	Leu	Val	Leu					
		1070				1075					1080								
Gln	Asp	Ala	Val	Ile	Thr	Ile	Thr												
		1085				1090													



<211> 1066  
 <212> PRT  
 <213> Unknown

<220>

<223> fungus sp. or fungus infected gracilariopsis sp.

<400> 3

Met	Ala	Gly	Phe	Ser	Asp	Pro	Leu	Asn	Phe	Cys	Lys	Ala	Glu	Asp	Tyr	1	5	10	15
Tyr	Ser	Val	Ala	Leu	Asp	Trp	Lys	Gly	Pro	Gln	Lys	Ile	Ile	Gly	Val	20	25	30	
Asp	Thr	Thr	Pro	Pro	Lys	Ser	Thr	Lys	Phe	Pro	Lys	Asn	Trp	His	Gly	35	40	45	
Val	Asn	Leu	Arg	Phe	Asp	Asp	Gly	Thr	Leu	Gly	Val	Val	Gln	Phe	Ile	50	55	60	
Arg	Pro	Cys	Val	Trp	Arg	Val	Arg	Tyr	Asp	Pro	Gly	Phe	Lys	Thr	Ser	65	70	75	80
Asp	Glu	Tyr	Gly	Asp	Glu	Asn	Thr	Arg	Thr	Ile	Val	Gln	Asp	Tyr	Met	85	90	95	
Ser	Thr	Leu	Ser	Asn	Lys	Leu	Asp	Thr	Tyr	Arg	Gly	Leu	Thr	Trp	Glu	100	105	110	
Thr	Lys	Cys	Glu	Asp	Ser	Gly	Asp	Phe	Phe	Thr	Phe	Ser	Ser	Lys	Val	115	120	125	
Thr	Ala	Val	Glu	Lys	Ser	Glu	Arg	Thr	Arg	Asn	Lys	Val	Gly	Asp	Gly	130	135	140	
Leu	Arg	Ile	His	Leu	Trp	Lys	Ser	Pro	Phe	Arg	Ile	Gln	Val	Val	Arg	145	150	155	160
Thr	Leu	Thr	Pro	Leu	Lys	Asp	Pro	Tyr	Pro	Ile	Pro	Asn	Val	Ala	Ala	165	170	175	
Ala	Glu	Ala	Arg	Val	Ser	Asp	Lys	Val	Val	Trp	Gln	Thr	Ser	Pro	Lys	180	185	190	
Thr	Phe	Arg	Lys	Asn	Leu	His	Pro	Gln	His	Lys	Met	Leu	Lys	Asp	Thr	195	200	205	
Val	Leu	Asp	Ile	Val	Lys	Pro	Gly	His	Gly	Glu	Tyr	Val	Gly	Trp	Gly	210	215	220	
Glu	Met	Gly	Gly	Ile	Gln	Phe	Met	Lys	Glu	Pro	Thr	Phe	Met	Asn	Tyr	225	230	235	240
Phe	Asn	Phe	Asp	Asn	Met	Gln	Tyr	Gln	Gln	Val	Tyr	Ala	Gln	Gly	Ala	245	250	255	

Leu Asp Ser Arg Glu Pro Leu Tyr His Ser Asp Pro Phe Tyr Leu Asp  
 260 265 270  
 Val Asn Ser Asn Pro Glu His Lys Asn Ile Thr Ala Thr Phe Ile Asp  
 275 280 285  
 Asn Tyr Ser Gln Ile Ala Ile Asp Phe Gly Lys Thr Asn Ser Gly Tyr  
 290 295 300  
 Ile Lys Leu Gly Thr Arg Tyr Gly Gly Ile Asp Cys Tyr Gly Ile Ser  
 305 310 315 320  
 Ala Asp Thr Val Pro Glu Ile Val Arg Leu Tyr Thr Gly Leu Val Gly  
 325 330 335  
 Arg Ser Lys Leu Lys Pro Arg Tyr Ile Leu Gly Ala His Gln Ala Cys  
 340 345 350  
 Tyr Gly Tyr Gln Gln Glu Ser Asp Leu Tyr Ser Val Val Gln Gln Tyr  
 355 360 365  
 Arg Asp Cys Lys Phe Pro Leu Asp Gly Ile His Val Asp Val Asp Val  
 370 375 380  
 Gln Asp Gly Phe Arg Thr Phe Thr Thr Asn Pro His Thr Phe Pro Asn  
 385 390 395 400  
 Pro Lys Glu Met Phe Thr Asn Leu Arg Asn Asn Gly Ile Lys Cys Ser  
 405 410 415  
 Thr Asn Ile Thr Pro Val Ile Ser Ile Asn Asn Arg Glu Gly Gly Tyr  
 420 425 430  
 Ser Thr Leu Leu Glu Gly Val Asp Lys Lys Tyr Phe Ile Met Asp Asp  
 435 440 445  
 Arg Tyr Thr Glu Gly Thr Ser Gly Asn Ala Lys Asp Val Arg Tyr Met  
 450 455 460  
 Tyr Tyr Gly Gly Gly Asn Lys Val Glu Val Asp Pro Asn Asp Val Asn  
 465 470 475 480  
 Gly Arg Pro Asp Phe Lys Asp Asn Tyr Asp Phe Pro Ala Asn Phe Asn  
 485 490 495  
 Ser Lys Gln Tyr Pro Tyr His Gly Gly Val Ser Tyr Gly Tyr Gly Asn  
 500 505 510  
 Gly Ser Ala Gly Phe Tyr Pro Asp Leu Asn Arg Lys Glu Val Arg Ile  
 515 520 525  
 Trp Trp Gly Met Gln Tyr Lys Tyr Leu Phe Asp Met Gly Leu Glu Phe  
 530 535 540  
 Val Trp Gln Asp Met Thr Thr Pro Ala Ile His Thr Ser Tyr Gly Asp  
 545 550 555 560

Met	Lys	Gly	Leu	Pro	Thr	Arg	Leu	Leu	Val	Thr	Ser	Asp	Ser	Val	Thr	565	570	575
Asn	Ala	Ser	Glu	Lys	Lys	Leu	Ala	Ile	Glu	Thr	Trp	Ala	Leu	Tyr	Ser	580	585	590
Tyr	Asn	Leu	His	Lys	Ala	Thr	Trp	His	Gly	Leu	Ser	Arg	Leu	Glu	Ser	595	600	605
Arg	Lys	Asn	Lys	Arg	Asn	Phe	Ile	Leu	Gly	Arg	Gly	Ser	Tyr	Ala	Gly	610	615	620
Ala	Tyr	Arg	Phe	Ala	Gly	Leu	Trp	Thr	Gly	Asp	Asn	Ala	Ser	Asn	Trp	625	630	635
Glu	Phe	Trp	Lys	Ile	Ser	Val	Ser	Gln	Val	Leu	Ser	Leu	Gly	Leu	Asn	645	650	655
Gly	Val	Cys	Ile	Ala	Gly	Ser	Asp	Thr	Gly	Gly	Phe	Glu	Pro	Tyr	Arg	660	665	670
Asp	Ala	Asn	Gly	Val	Glu	Glu	Lys	Tyr	Cys	Ser	Pro	Glu	Leu	Leu	Ile	675	680	685
Arg	Trp	Tyr	Thr	Gly	Ser	Phe	Leu	Leu	Pro	Trp	Leu	Arg	Asn	His	Tyr	690	695	700
Val	Lys	Lys	Asp	Arg	Lys	Trp	Phe	Gln	Glu	Pro	Tyr	Ser	Tyr	Pro	Lys	705	710	715
His	Leu	Glu	Thr	His	Pro	Glu	Leu	Ala	Asp	Gln	Ala	Trp	Leu	Tyr	Lys	725	730	735
Ser	Val	Leu	Glu	Ile	Cys	Arg	Tyr	Tyr	Val	Glu	Leu	Arg	Tyr	Ser	Leu	740	745	750
Ile	Gln	Leu	Leu	Tyr	Asp	Cys	Met	Phe	Gln	Asn	Val	Val	Asp	Gly	Met	755	760	765
Pro	Ile	Thr	Arg	Ser	Met	Leu	Leu	Thr	Asp	Thr	Glu	Asp	Thr	Thr	Phe	770	775	780
Phe	Asn	Glu	Ser	Gln	Lys	Phe	Leu	Asp	Asn	Gln	Tyr	Met	Ala	Gly	Asp	785	790	795
Asp	Ile	Leu	Val	Ala	Pro	Ile	Leu	His	Ser	Arg	Lys	Glu	Ile	Pro	Gly	805	810	815
Glu	Asn	Arg	Asp	Val	Tyr	Leu	Pro	Leu	Tyr	His	Thr	Trp	Tyr	Pro	Ser	820	825	830
Asn	Leu	Arg	Pro	Trp	Asp	Asp	Gln	Gly	Val	Ala	Leu	Gly	Asn	Pro	Val	835	840	845
Glu	Gly	Gly	Ser	Val	Ile	Asn	Tyr	Thr	Ala	Arg	Ile	Val	Ala	Pro	Glu	850	855	860

Asp Tyr Asn Leu Phe His Ser Val Val Pro Val Tyr Val Arg Glu Gly  
 865 870 875 880  
 Ala Ile Ile Pro Gln Ile Glu Val Arg Gln Trp Thr Gly Gln Gly Gly  
 885 890 895  
 Ala Asn Arg Ile Lys Phe Asn Ile Tyr Pro Gly Lys Asp Lys Glu Tyr  
 900 905 910  
 Cys Thr Tyr Leu Asp Asp Gly Val Ser Arg Asp Ser Ala Pro Glu Asp  
 915 920 925  
 Leu Pro Gln Tyr Lys Glu Thr His Glu Gln Ser Lys Val Glu Gly Ala  
 930 935 940  
 Glu Ile Ala Lys Gln Ile Gly Lys Lys Thr Gly Tyr Asn Ile Ser Gly  
 945 950 955 960  
 Thr Asp Pro Glu Ala Lys Gly Tyr His Arg Lys Val Ala Val Thr Gln  
 965 970 975  
 Thr Ser Lys Asp Lys Thr Arg Thr Val Thr Ile Glu Pro Lys His Asn  
 980 985 990  
 Gly Tyr Asp Pro Ser Lys Glu Val Gly Asp Tyr Tyr Thr Ile Ile Leu  
 995 1000 1005  
 Trp Tyr Ala Pro Gly Phe Asp Gly Ser Ile Val Asp Val Ser Lys  
 1010 1015 1020  
 Thr Thr Val Asn Val Glu Gly Gly Val Glu His Gln Val Tyr Lys  
 1025 1030 1035  
 Asn Ser Asp Leu His Thr Val Val Ile Asp Val Lys Glu Val Ile  
 1040 1045 1050  
 Gly Thr Thr Lys Ser Val Lys Ile Thr Cys Thr Ala Ala  
 1055 1060 1065  
 <210> 4  
 <211> 1070  
 <212> PRT  
 <213> Unknown  
 <220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.  
 <400> 4  
 Met Ala Gly Leu Ser Asp Pro Leu Asn Phe Cys Lys Ala Glu Asp Tyr  
 1 5 10 15  
 Tyr Ala Ala Ala Lys Gly Trp Ser Gly Pro Gln Lys Ile Ile Arg Tyr  
 20 25 30  
 Asp Gln Thr Pro Pro Gln Gly Thr Lys Asp Pro Lys Ser Trp His Ala  
 35 40 45

Val	Asn	Leu	Pro	Phe	Asp	Asp	Gly	Thr	Met	Cys	Val	Val	Gln	Phe	Val	50	55	60	
Arg	Pro	Cys	Val	Trp	Arg	Val	Arg	Tyr	Asp	Pro	Ser	Val	Lys	Thr	Ser	65	70	75	80
Asp	Glu	Tyr	Gly	Asp	Glu	Asn	Thr	Arg	Thr	Ile	Val	Gln	Asp	Tyr	Met	85	90	95	
Thr	Thr	Leu	Val	Gly	Asn	Leu	Asp	Ile	Phe	Arg	Gly	Leu	Thr	Trp	Val	100	105	110	
Ser	Thr	Leu	Glu	Asp	Ser	Gly	Glu	Tyr	Tyr	Thr	Phe	Lys	Ser	Glu	Val	115	120	125	
Thr	Ala	Val	Asp	Glu	Thr	Glu	Arg	Thr	Arg	Asn	Lys	Val	Gly	Asp	Gly	130	135	140	
Leu	Lys	Ile	Tyr	Leu	Trp	Lys	Asn	Pro	Phe	Arg	Ile	Gln	Val	Val	Arg	145	150	155	160
Leu	Leu	Thr	Pro	Leu	Val	Asp	Pro	Phe	Pro	Ile	Pro	Asn	Val	Ala	Asn	165	170	175	
Ala	Thr	Ala	Arg	Val	Ala	Asp	Lys	Val	Val	Trp	Gln	Thr	Ser	Pro	Lys	180	185	190	
Thr	Phe	Arg	Lys	Asn	Leu	His	Pro	Gln	His	Lys	Met	Leu	Lys	Asp	Thr	195	200	205	
Val	Leu	Asp	Ile	Ile	Lys	Pro	Gly	His	Gly	Glu	Tyr	Val	Gly	Trp	Gly	210	215	220	
Glu	Met	Gly	Gly	Ile	Glu	Phe	Met	Lys	Glu	Pro	Thr	Phe	Met	Asn	Tyr	225	230	235	240
Phe	Asn	Phe	Asp	Asn	Met	Gln	Tyr	Gln	Gln	Val	Tyr	Ala	Gln	Gly	Ala	245	250	255	
Leu	Asp	Ser	Arg	Glu	Pro	Leu	Tyr	His	Ser	Asp	Pro	Phe	Tyr	Leu	Asp	260	265	270	
Val	Asn	Ser	Asn	Pro	Glu	His	Lys	Asn	Ile	Thr	Ala	Thr	Phe	Ile	Asp	275	280	285	
Asn	Tyr	Ser	Gln	Ile	Ala	Ile	Asp	Phe	Gly	Lys	Thr	Asn	Ser	Gly	Tyr	290	295	300	
Ile	Lys	Leu	Gly	Thr	Arg	Tyr	Gly	Gly	Ile	Asp	Cys	Tyr	Gly	Ile	Ser	305	310	315	320
Ala	Asp	Thr	Val	Pro	Glu	Ile	Val	Arg	Leu	Tyr	Thr	Gly	Leu	Val	Gly	325	330	335	
Arg	Ser	Lys	Leu	Lys	Pro	Arg	Tyr	Ile	Leu	Gly	Ala	His	Gln	Ala	Cys	340	345	350	

Tyr Gly Tyr Gln Gln Glu Ser Asp Leu His Ala Val Val Gln Gln Tyr  
 355 360 365  
 Arg Asp Thr Lys Phe Pro Leu Asp Gly Leu His Val Asp Val Asp Phe  
 370 375 380  
 Gln Asp Asn Phe Arg Thr Phe Thr Thr Asn Pro Ile Thr Phe Pro Asn  
 385 390 395 400  
 Pro Lys Glu Met Phe Thr Asn Leu Arg Asn Asn Gly Ile Lys Cys Ser  
 405 410 415  
 Thr Asn Ile Thr Pro Val Ile Ser Ile Arg Asp Arg Pro Asn Gly Tyr  
 420 425 430  
 Ser Thr Leu Asn Glu Gly Tyr Asp Lys Lys Tyr Phe Ile Met Asp Asp  
 435 440 445  
 Arg Tyr Thr Glu Gly Thr Ser Gly Asp Pro Gln Asn Val Arg Tyr Ser  
 450 455 460  
 Phe Tyr Gly Gly Gly Asn Pro Val Glu Val Asn Pro Asn Asp Val Trp  
 465 470 475 480  
 Ala Arg Pro Asp Phe Gly Asp Asn Tyr Asp Phe Pro Thr Asn Phe Asn  
 485 490 495  
 Cys Lys Asp Tyr Pro Tyr His Gly Gly Val Ser Tyr Gly Tyr Gly Asn  
 500 505 510  
 Gly Thr Pro Gly Tyr Tyr Pro Asp Leu Asn Arg Glu Glu Val Arg Ile  
 515 520 525  
 Trp Trp Gly Leu Gln Tyr Glu Tyr Leu Phe Asn Met Gly Leu Glu Phe  
 530 535 540  
 Val Trp Gln Asp Met Thr Thr Pro Ala Ile His Ser Ser Tyr Gly Asp  
 545 550 555 560  
 Met Lys Gly Leu Pro Thr Arg Leu Leu Val Thr Ala Asp Ser Val Thr  
 565 570 575  
 Asn Ala Ser Glu Lys Lys Leu Ala Ile Glu Ser Trp Ala Leu Tyr Ser  
 580 585 590  
 Tyr Asn Leu His Lys Ala Thr Phe His Gly Leu Gly Arg Leu Glu Ser  
 595 600 605  
 Arg Lys Asn Lys Arg Asn Phe Ile Leu Gly Arg Gly Ser Tyr Ala Gly  
 610 615 620  
 Ala Tyr Arg Phe Ala Gly Leu Trp Thr Gly Asp Asn Ala Ser Thr Trp  
 625 630 635 640  
 Glu Phe Trp Lys Ile Ser Val Ser Gln Val Leu Ser Leu Gly Leu Asn  
 645 650 655

Gly Val Cys Ile Ala Gly Ser Asp Thr Gly Gly Phe Glu Pro Ala Arg  
 660 665 670  
 Thr Glu Ile Gly Glu Glu Lys Tyr Cys Ser Pro Glu Leu Leu Ile Arg  
 675 680 685  
 Trp Tyr Thr Gly Ser Phe Leu Leu Pro Trp Leu Arg Asn His Tyr Val  
 690 695 700  
 Lys Lys Asp Arg Lys Trp Phe Gln Glu Pro Tyr Ala Tyr Pro Lys His  
 705 710 715 720  
 Leu Glu Thr His Pro Glu Leu Ala Asp Gln Ala Trp Leu Tyr Lys Ser  
 725 730 735  
 Val Leu Glu Ile Cys Arg Tyr Trp Val Glu Leu Arg Tyr Ser Leu Ile  
 740 745 750  
 Gln Leu Leu Tyr Asp Cys Met Phe Gln Asn Val Val Asp Gly Met Pro  
 755 760 765  
 Leu Ala Arg Ser Met Leu Leu Thr Asp Thr Glu Asp Thr Thr Phe Phe  
 770 775 780  
 Asn Glu Ser Gln Lys Phe Leu Asp Asn Gln Tyr Met Ala Gly Asp Asp  
 785 790 795 800  
 Ile Leu Val Ala Pro Ile Leu His Ser Arg Asn Glu Val Pro Gly Glu  
 805 810 815  
 Asn Arg Asp Val Tyr Leu Pro Leu Phe His Thr Trp Tyr Pro Ser Asn  
 820 825 830  
 Leu Arg Pro Trp Asp Asp Gln Gly Val Ala Leu Gly Asn Pro Val Glu  
 835 840 845  
 Gly Gly Ser Val Ile Asn Tyr Thr Ala Arg Ile Val Ala Pro Glu Asp  
 850 855 860  
 Tyr Asn Leu Phe His Asn Val Val Pro Val Tyr Ile Arg Glu Gly Ala  
 865 870 875 880  
 Ile Ile Pro Gln Ile Gln Val Arg Gln Trp Ile Gly Glu Gly Gly Pro  
 885 890 895  
 Asn Pro Ile Lys Phe Asn Ile Tyr Pro Gly Lys Asp Lys Glu Tyr Val  
 900 905 910  
 Thr Tyr Leu Asp Asp Gly Val Ser Arg Asp Ser Ala Pro Asp Asp Leu  
 915 920 925  
 Pro Gln Tyr Arg Glu Ala Tyr Glu Gln Ala Lys Val Glu Gly Lys Asp  
 930 935 940  
 Val Gln Lys Gln Leu Ala Val Ile Gln Gly Asn Lys Thr Asn Asp Phe  
 945 950 955 960

Ser Ala Ser Gly Ile Asp Lys Glu Ala Lys Gly Tyr His Arg Lys Val  
                           965                          970                          975

Ser Ile Lys Gln Glu Ser Lys Asp Lys Thr Arg Thr Val Thr Ile Glu  
                           980                          985                          990

Pro Lys His Asn Gly Tyr Asp Pro Ser Lys Glu Val Gly Asn Tyr Tyr  
                           995                          1000                          1005

Thr Ile Ile Leu Trp Tyr Ala Pro Gly Phe Asp Gly Ser Ile Val  
                           1010                          1015                          1020

Asp Val Ser Gln Ala Thr Val Asn Ile Glu Gly Gly Val Glu Cys  
                           1025                          1030                          1035

Glu Ile Phe Lys Asn Thr Gly Leu His Thr Val Val Val Asn Val  
                           1040                          1045                          1050

Lys Glu Val Ile Gly Thr Thr Lys Ser Val Lys Ile Thr Cys Thr  
                           1055                          1060                          1065

Thr Ala  
           1070

<210> 5  
 <211> 1092  
 <212> PRT  
 <213> Unknown

<220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.

<400> 5

Met Phe Pro Thr Leu Thr Phe Ile Ala Pro Ser Ala Leu Ala Ala Ser  
 1                          5                          10                          15

Thr Phe Val Gly Ala Asp Ile Arg Ser Gly Ile Arg Ile Gln Ser Ala  
                           20                          25                          30

Leu Pro Ala Val Arg Asn Ala Val Arg Arg Ser Lys His Tyr Asn Val  
                           35                          40                          45

Ser Met Thr Ala Leu Ser Asp Lys Gln Thr Ala Ile Ser Ile Gly Pro  
                           50                          55                          60

Asp Asn Pro Asp Gly Ile Asn Tyr Gln Asn Tyr Asp Tyr Ile Pro Val  
 65                          70                          75                          80

Ala Gly Phe Thr Pro Leu Ser Asn Thr Asn Trp Tyr Ala Ala Gly Ser  
                           85                          90                          95

Ser Thr Pro Gly Gly Ile Thr Asp Trp Thr Ala Thr Met Asn Val Lys  
                           100                          105                          110

Phe Asp Arg Ile Asp Asn Pro Ser Tyr Ser Asn Asn His Pro Val Gln



115					120					125					
Ile	Gln	Val	Thr	Ser	Tyr	Asn	Asn	Asn	Ser	Phe	Arg	Ile	Arg	Phe	Asn
130						135					140				
Pro	Asp	Gly	Pro	Ile	Arg	Asp	Val	Ser	Arg	Gly	Pro	Ile	Leu	Lys	Gln
145						150					155				160
Gln	Leu	Thr	Trp	Ile	Arg	Asn	Gln	Glu	Leu	Ala	Gln	Gly	Cys	Asn	Pro
				165					170					175	
Asn	Met	Ser	Phe	Ser	Pro	Glu	Gly	Phe	Leu	Ser	Phe	Glu	Thr	Lys	Asp
			180					185					190		
Leu	Asn	Val	Ile	Ile	Tyr	Gly	Asn	Cys	Lys	Met	Arg	Val	Thr	Lys	Lys
		195					200					205			
Asp	Gly	Tyr	Leu	Val	Met	Glu	Asn	Asp	Glu	Cys	Asn	Ser	Gln	Ser	Asp
	210					215					220				
Gly	Asn	Lys	Cys	Arg	Gly	Leu	Met	Tyr	Val	Asp	Arg	Leu	Tyr	Gly	Asn
225						230					235				240
Ala	Ile	Ala	Ser	Val	Gln	Thr	Asn	Phe	His	Lys	Asp	Thr	Ser	Arg	Asn
			245						250					255	
Glu	Lys	Phe	Tyr	Gly	Ala	Gly	Glu	Val	Asn	Cys	Arg	Tyr	Glu	Glu	Gln
			260					265					270		
Gly	Lys	Ala	Pro	Thr	Tyr	Val	Leu	Glu	Arg	Ser	Gly	Leu	Ala	Met	Thr
	275						280					285			
Asn	Tyr	Asn	Tyr	Asp	Asn	Leu	Asn	Tyr	Asn	Gln	Pro	Asp	Val	Val	Pro
	290					295					300				
Pro	Gly	Tyr	Pro	Asp	His	Pro	Asn	Tyr	Tyr	Ile	Pro	Met	Tyr	Tyr	Ala
305						310					315				320
Ala	Pro	Trp	Leu	Val	Val	Gln	Gly	Cys	Ala	Gly	Thr	Ser	Lys	Gln	Tyr
			325						330					335	
Ser	Tyr	Gly	Trp	Phe	Met	Asp	Asn	Val	Ser	Gln	Ser	Tyr	Met	Asn	Thr
			340					345					350		
Gly	Asp	Thr	Ala	Trp	Asn	Cys	Gly	Gln	Glu	Asn	Leu	Ala	Tyr	Met	Gly
	355						360					365			
Ala	Gln	Tyr	Gly	Pro	Phe	Asp	Gln	His	Phe	Val	Tyr	Gly	Asp	Gly	Asp
	370					375					380				
Gly	Leu	Glu	Asp	Val	Val	Lys	Ala	Phe	Ser	Phe	Leu	Gln	Gly	Lys	Glu
385						390					395				400
Phe	Glu	Asp	Lys	Lys	Leu	Asn	Lys	Arg	Ser	Val	Met	Pro	Pro	Lys	Tyr
			405						410					415	
Val	Phe	Gly	Phe	Phe	Gln	Gly	Val	Phe	Gly	Ala	Leu	Ser	Leu	Leu	Lys

420					425					430						
Gln	Asn	Leu	Pro	Ala	Gly	Glu	Asn	Asn	Ile	Ser	Val	Gln	Glu	Ile	Val	
435					440					445						
Glu	Gly	Tyr	Gln	Asp	Asn	Asp	Tyr	Pro	Phe	Glu	Gly	Leu	Ala	Val	Asp	
450					455					460						
Val	Asp	Met	Gln	Asp	Asp	Leu	Arg	Val	Phe	Thr	Thr	Lys	Pro	Glu	Tyr	
465					470					475					480	
Trp	Ser	Ala	Asn	Met	Val	Gly	Glu	Gly	Gly	Asp	Pro	Asn	Asn	Arg	Ser	
485					490					495						
Val	Phe	Glu	Trp	Ala	His	Asp	Arg	Gly	Leu	Val	Cys	Gln	Thr	Asn	Val	
500					505					510						
Thr	Cys	Phe	Leu	Arg	Asn	Asp	Asn	Ser	Gly	Lys	Pro	Tyr	Glu	Val	Asn	
515					520					525						
Gln	Thr	Leu	Arg	Glu	Lys	Gln	Leu	Tyr	Thr	Lys	Asn	Asp	Ser	Leu	Asn	
530					535					540						
Asn	Thr	Asp	Phe	Gly	Thr	Thr	Ser	Asp	Gly	Pro	Gly	Asp	Ala	Tyr	Ile	
545					550					555					560	
Gly	His	Leu	Asp	Tyr	Gly	Gly	Gly	Val	Glu	Cys	Asp	Ala	Ile	Phe	Pro	
565					570					575						
Asp	Trp	Gly	Arg	Pro	Asp	Val	Ala	Gln	Trp	Trp	Gly	Glu	Asn	Tyr	Lys	
580					585					590						
Lys	Leu	Phe	Ser	Ile	Gly	Leu	Asp	Phe	Val	Trp	Gln	Asp	Met	Thr	Val	
595					600					605						
Pro	Ala	Met	Met	Pro	His	Arg	Leu	Gly	Asp	Ala	Val	Asn	Lys	Asn	Ser	
610					615					620						
Gly	Ser	Ser	Ala	Pro	Gly	Trp	Pro	Asn	Glu	Asn	Asp	Pro	Ser	Asn	Gly	
625					630					635					640	
Arg	Tyr	Asn	Trp	Lys	Ser	Tyr	His	Pro	Gln	Val	Leu	Val	Thr	Asp	Met	
645					650					655						
Arg	Tyr	Gly	Ala	Glu	Tyr	Gly	Arg	Glu	Pro	Met	Val	Ser	Gln	Arg	Asn	
660					665					670						
Ile	His	Ala	Tyr	Thr	Leu	Cys	Glu	Ser	Thr	Arg	Arg	Glu	Gly	Ile	Val	
675					680					685						
Gly	Asn	Ala	Asp	Ser	Leu	Thr	Lys	Phe	Arg	Arg	Ser	Tyr	Ile	Ile	Ser	
690					695					700						
Arg	Gly	Gly	Tyr	Ile	Gly	Asn	Gln	His	Phe	Gly	Gly	Met	Trp	Val	Gly	
705					710					715					720	
Asp	Asn	Ser	Ala	Thr	Glu	Ser	Tyr	Leu	Gln	Met	Met	Leu	Ala	Asn	Ile	

725										730					735				
Ile	Asn	Met	Asn	Met	Ser	Cys	Leu	Pro	Leu	Val	Gly	Ser	Asp	Ile	Gly				
			740					745					750						
Gly	Phe	Thr	Gln	Tyr	Asn	Asp	Ala	Gly	Asp	Pro	Thr	Pro	Glu	Asp	Leu				
		755					760						765						
Met	Val	Arg	Phe	Val	Gln	Ala	Gly	Cys	Leu	Leu	Pro	Trp	Phe	Arg	Asn				
		770				775						780							
His	Tyr	Asp	Arg	Trp	Ile	Glu	Ser	Lys	Lys	His	Gly	Lys	Lys	Tyr	Gln				
785					790					795					800				
Glu	Leu	Tyr	Met	Tyr	Pro	Gly	Gln	Lys	Asp	Thr	Leu	Lys	Lys	Phe	Val				
				805					810					815					
Glu	Phe	Arg	Tyr	Arg	Trp	Gln	Glu	Val	Leu	Tyr	Thr	Ala	Met	Tyr	Gln				
			820					825					830						
Asn	Ala	Thr	Thr	Gly	Glu	Pro	Ile	Ile	Lys	Ala	Ala	Pro	Met	Tyr	Asn				
		835					840					845							
Asn	Asp	Val	Asn	Val	Tyr	Lys	Ser	Gln	Asn	Asp	His	Phe	Leu	Leu	Gly				
		850				855					860								
Gly	His	Asp	Gly	Tyr	Arg	Ile	Leu	Cys	Ala	Pro	Val	Val	Arg	Glu	Asn				
865					870					875					880				
Ala	Thr	Ser	Arg	Glu	Val	Tyr	Leu	Pro	Val	Tyr	Ser	Lys	Trp	Phe	Lys				
			885						890					895					
Phe	Gly	Pro	Asp	Phe	Asp	Thr	Lys	Pro	Leu	Glu	Asn	Glu	Ile	Gln	Gly				
			900					905					910						
Gly	Gln	Thr	Leu	Tyr	Asn	Tyr	Ala	Ala	Pro	Leu	Asn	Asp	Ser	Pro	Ile				
		915					920					925							
Phe	Val	Arg	Glu	Gly	Thr	Ile	Leu	Pro	Thr	Arg	Tyr	Thr	Leu	Asp	Gly				
		930				935					940								
Val	Asn	Lys	Ser	Ile	Asn	Thr	Tyr	Thr	Asp	Asn	Asp	Pro	Leu	Val	Phe				
945					950					955					960				
Glu	Leu	Phe	Pro	Leu	Glu	Asn	Asn	Gln	Ala	His	Gly	Leu	Phe	Tyr	His				
			965					970						975					
Asp	Asp	Gly	Gly	Val	Thr	Thr	Asn	Ala	Glu	Asp	Phe	Gly	Lys	Tyr	Ser				
			980					985					990						
Val	Ile	Ser	Val	Lys	Ala	Ala	Gln	Glu	Gly	Ser	Gln	Met	Ser	Val	Lys				
		995					1000					1005							
Phe	Asp	Asn	Glu	Val	Tyr	Glu	His	Gln	Trp	Gly	Ala	Ser	Phe	Tyr					
	1010					1015					1020								
Val	Arg	Val	Arg	Asn	Met	Gly	Ala	Pro	Ser	Asn	Ile	Asn	Val	Ser					

1025                      1030                      1035  
 Ser Gln Ile Gly Gln Gln Asp Met Gln Gln Ser Ser Val Ser Ser  
 1040                      1045                      1050  
 Arg Ala Gln Met Phe Thr Ser Ala Asn Asp Gly Glu Tyr Trp Val  
 1055                      1060                      1065  
 Asp Gln Ser Thr Asn Ser Leu Trp Leu Lys Leu Pro Gly Ala Val  
 1070                      1075                      1080  
 Ile Gln Asp Ala Ala Ile Thr Val Arg  
 1085                      1090  
 <210> 6  
 <211> 570  
 <212> PRT  
 <213> Unknown  
 <220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.  
 <400> 6  
 Met Thr Asn Tyr Asn Tyr Asp Asn Leu Asn Tyr Asn Gln Pro Asp Leu  
 1                      5                      10                      15  
 Ile Pro Pro Gly His Asp Ser Asp Pro Asp Tyr Tyr Ile Pro Met Tyr  
 20                      25                      30  
 Phe Ala Ala Pro Trp Val Ile Ala His Gly Tyr Arg Gly Thr Ser Asp  
 35                      40                      45  
 Gln Tyr Ser Tyr Gly Trp Phe Leu Asp Asn Val Ser Gln Ser Tyr Thr  
 50                      55                      60  
 Asn Thr Gly Asp Asp Ala Trp Ala Gly Gln Lys Asp Leu Ala Tyr Met  
 65                      70                      75                      80  
 Gly Ala Gln Cys Gly Pro Phe Asp Gln His Phe Val Tyr Glu Ala Gly  
 85                      90                      95  
 Asp Gly Leu Glu Asp Val Val Thr Ala Phe Ser Tyr Leu Gln Gly Lys  
 100                      105                      110  
 Glu Tyr Glu Asn Gln Gly Leu Asn Ile Arg Ser Ala Met Pro Pro Lys  
 115                      120                      125  
 Tyr Val Phe Gly Phe Phe Gln Gly Val Phe Gly Ala Thr Ser Leu Leu  
 130                      135                      140  
 Arg Asp Asn Leu Pro Ala Gly Glu Asn Asn Val Ser Leu Glu Glu Ile  
 145                      150                      155                      160  
 Val Glu Gly Tyr Gln Asn Gln Asn Val Pro Phe Glu Gly Leu Ala Val  
 165                      170                      175



Phe Val Gln Ala Gly Cys Leu Leu Pro Trp Phe Arg Asn His Tyr Asp  
 485 490 495

Arg Trp Ile Glu Ser Lys Lys His Gly Lys Asn Tyr Gln Glu Leu Tyr  
 500 505 510

Met Tyr Arg Asp His Leu Asp Ala Leu Arg Ser Phe Val Glu Leu Arg  
 515 520 525

Tyr Arg Trp Gln Glu Val Leu Tyr Thr Ala Met Tyr Gln Asn Ala Leu  
 530 535 540

Asn Gly Lys Pro Ile Ile Lys Thr Val Ser Met Tyr Asn Asn Asp Met  
 545 550 555 560

Asn Val Lys Asp Ala Gln Asn Asp His Phe  
 565 570

<210> 7  
 <211> 3267  
 <212> DNA  
 <213> Unknown

<220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.

<400> 7  
 atgttttcaa cccttgcggt tgctgcacct agtgcgctgg gagccagtac cttcgtaggg 60  
 gcggagggtca ggtcaaatgt tcgtatccat tccgcttttc cagctgtgca cacagctact 120  
 cgcaaaacca atcgctcaa tgtatccatg accgcattgt ccgacaaaca aacggctact 180  
 gcgggtagta cagacaatcc ggacggtatc gactacaaga cctacgatta cgtcggagta 240  
 tggggtttca gccccctctc caacacgaac tggtttgctg ccggctcttc taccgccgggt 300  
 ggcactactg attggacggc tacaatgaat gtcaacttcg accgtatcga caatccgtcc 360  
 atcactgtcc agcatcccggt tcaggttcag gtcacgtcat acaacaaca cagctacagg 420  
 gttcgcttca accctgatgg ccctattcgt gatgtgactc gtgggcctat cctcaagcag 480  
 caactagatt ggattcgaac gcaggagctg tcagagggat gtgatcccg aatgactttc 540  
 acatcagaag gtttcttgac ttttgagacc aaggatctaa gcgtcatcat ctacggaaat 600  
 ttcaagacca gagttacgag aaagtctgac ggcaagggtca tcatggaaaa tgatgaagtt 660  
 ggaactgcat cgtccgggaa caagtgccgg ggattgatgt tcgttgatag attatacgggt 720  
 aacgctatcg cttccgtcaa caagaacttc cgcaacgacg cgggtcaagca ggagggattc 780  
 tatgggtgcag gtgaagtcaa ctgtaagtac caggacacct acatcttaga acgcactgga 840  
 atcgccatga caaattacaa ctacgataac ttgaactata accagtggga ccttagacct 900

cgcgcatcatg atgggtgccct caaccagac tattatattc caatgtacta cgcagcacct	960
tggttgatcg ttaatggatg cgccggtact tcggagcagt actcgtatgg atggttcatg	1020
gacaatgtct ctcaatctta catgaatact ggagatacta cctggaattc tggacaagag	1080
gacctggcat acatgggcgc gcagtatgga ccatttgacc aacattttgt ttacgggtgct	1140
gggggtggga tggaatgtgt ggtcacagcg ttctctcttc tacaaggcaa ggagttcgag	1200
aaccaagttc tcaacaaacg ttcagtaatg cctccgaaat acgtctttgg tttcttcag	1260
ggtgttttcg ggacttcttc cttgttgaga gcgcatatgc cagcaggtga gaacaacatc	1320
tcagtcgaag aaattgtaga aggttatcaa aacaacaatt tccctttcga ggggtcgcct	1380
gtggacgtgg atatgcaaga caacttgccg gtgttcacca cgaaggcgga attttgacc	1440
gcaaacaggg tggttactgg cggggatcca aacaaccgat cggtttttga atgggcacat	1500
gacaaaggcc ttgtttgtca gacaaatata acttgcttcc tgaggaatga taacgagggg	1560
caagactacg aggtcaatca gacgttaagg gagaggcagt tgtacacgaa gaacgactcc	1620
ctgacgggta cggattttgg aatgaccgac gacggcccca gcgatgcgta catcggtcat	1680
ctggactatg ggggtggagt agaatgtgat gcacttttcc cagactgggg acggcctgac	1740
gtggccgaat ggtggggaaa taactataag aaactgttca gcattggtct cgacttcgtc	1800
tggaagaca tgactgttcc agcaatgatg ccgcacaaaa ttggcgatga catcaatgtg	1860
aaaccggatg ggaattggcc gaatgcggac gatccgtcca atggacaata caactggaag	1920
acgtaccatc cccaagtgct tgtaactgat atgcgttatg agaatcatgg tcgggaaccg	1980
atggtcactc aacgcaacat tcatgcgtat acactgtgcg agtctactag gaaggaaggg	2040
atcgtggaaa acgcagacac tctaacgaag ttccgccgta gctacattat cagtcgtggt	2100
ggttacattg gtaaccagca tttcgggggt atgtgggtgg gagacaactc tactacatca	2160
aactacatcc aaatgatgat tgccaacaat attaacatga atatgtcttg cttgcctctc	2220
gtcggctccg acattggagg attcacctca tacgacaatg agaatcagcg aacgccgtgt	2280
accggggact tgatggtgag gtatgtgcag gcgggctgcc tgttgccgtg gttcaggaac	2340
cactatgata ggtggatcga gtccaaggac cacggaaagg actaccagga gctgtacatg	2400
tatccgaatg aaatggatac gttgaggaag ttcgttgaat tccgttatcg ctggcaggaa	2460
gtgttgatca cggccatgta ccagaatgcg gctttcggaa agccgattat caaggctgct	2520
tcgatgtaca ataacgactc aaacgttcgc agggcgcaga acgatcattt ctttcttggg	2580
ggacatgatg gatatcgcat tctgtgcgcg cctgttgtgt gggagaattc gaccgaacgc	2640

gaattgtact tgcccggtgct gacccaatgg tacaaattcg gtcccgactt tgacaccaag 2700  
 cctctggaag gagcgatgaa cggagggggac cgaatttaca actaccctgt accgcaaagt 2760  
 gaatcaccaa tcttcgtgag agaaggtgag attctcccta cccgctacac gttgaacggt 2820  
 gaaaacaaat cattgaacac gtacacggac gaagatccgt tgggtgtttga agtattcccc 2880  
 ctccgaaaaca accgtgccga cggatatgtgt tatcttgatg atggcgggtgt gaccaccaat 2940  
 gctgaagaca atggcaagtt ctctgtcgtc aagggtggcag cggagcagga tgggtggtacg 3000  
 gagacgataa cgtttacgaa tgattgctat gagtacgttt tcggtggacc gttctacgtt 3060  
 cgagtgcgag gcgctcagtc gccgtcgaac atccacgtgt cttctggagc gggttctcag 3120  
 gacatgaagg tgagctctgc cacttccagg gctgcgctgt tcaatgacgg ggagaacggt 3180  
 gatttctggg ttgaccagga gacagattct ctgtggctga agttgccaa cgttggtctc 3240  
 ccggacgctg tgatcacaat tacctaa 3267

<210> 8  
 <211> 3276  
 <212> DNA  
 <213> Unknown

<220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.

<400> 8  
 atgtatccaa ccctcacctt cgtggcgct agtgcgctag gggccagaac tttcacgtgt 60  
 gtgggcattt ttaggtcaca cattcttatt cattcggttg ttccagcggg gcgtctagct 120  
 gtgcgcaaaa gcaaccgcct caatgtatcc atgtccgctt tgttcgacaa accgactgct 180  
 gttactggag ggaaggacaa cccggacaat atcaattaca ccacttatga ctacgtccct 240  
 gtgtggcgct tcgaccccct cagcaatacg aactggtttg ctgccggatc ttccactccc 300  
 ggcgatattg acgactggac ggcgacaatg aatgtgaact tcgaccgtat cgacaatcca 360  
 tccttcactc tcgagaaaacc ggttcagggt caggtcacgt catacaagaa caattgtttc 420  
 agggttcgct tcaaccctga tggtcctatt cgcgatgtgg atcgtggggc tatectccag 480  
 cagcaactaa attggatccg gaagcaggag cagtcgaagg ggtttgatcc taagatgggc 540  
 ttcacaaaag aagggtttctt gaaatttgag accaaggatc tgaacgttat catatatggc 600  
 aattttaaga ctagagttac gaggaagagg gatggaaaag ggatcatgga gaataatgaa 660  
 gtgccggcag gatcggttagg gaacaagtgc cggggattga tgtttgtcga cagggtgtac 720



ggcactgcc	tcgcttccgt	taatgaaaat	taccgcaacg	atccccgacag	gaaagagggg	780
ttctatggtg	caggagaagt	aaactgcgag	ttttgggact	ccgaacaaaa	caggaacaag	840
tacatcttag	aacgaactgg	aatcgccatg	acaaattaca	attatgacaa	ctataactac	900
aaccagtcag	atcttattgc	tccaggatat	ccttccgacc	cgaacttcta	cattcccatg	960
tattttgcag	caccttgggt	agttgttaag	ggatgcagtg	gcaacagcga	tgaacagtac	1020
tcgtacggat	ggtttatgga	taatgtctcc	caaacttaca	tgaatactgg	tggtacttcc	1080
tggaactgtg	gagaggagaa	cttggcatac	atgggagcac	agtgcggtcc	atttgaccaa	1140
cattttgtgt	atggtgatgg	agatgggtctt	gaggatgttg	tccaagcgtt	ctctcttctg	1200
caaggcaaag	agtttgagaa	ccaagttctg	aacaaacgtg	ccgtaatgcc	tccgaaatat	1260
gtgtttgggt	actttcaggg	agtctttggg	attgcttctt	tgttgagaga	gcaaagacca	1320
gagggtggtg	ataacatctc	tgttcaagag	attgtcgaag	gttaccaaag	caataacttc	1380
ccttttagagg	ggttagccgt	agatgtggat	atgcaacaag	atttgcgctg	gttcaccacg	1440
aagattgaat	tttgacggc	aaataaggta	ggcaccgggg	gagactcgaa	taacaagtcg	1500
gtgtttgaat	gggcacatga	caaaggcctt	gtatgtcaga	cgaatgttac	ttgcttcttg	1560
agaaacgaca	acggcggggc	agattacgaa	gtcaatcaga	cattgaggga	gaagggtttg	1620
tacacgaaga	atgactcact	gacgaacact	aacttcggaa	ctaccaacga	cgggccgagc	1680
gatgcgtaca	ttggacatct	ggactatggt	ggcggaggga	attgtgatgc	acttttccca	1740
gactggggtc	gaccgggtgt	ggctgaatgg	tggggtgata	actacagcaa	gctcttcaaa	1800
attggtctgg	atttcgtctg	gcaagacatg	acagttccag	ctatgatgcc	acacaaagtt	1860
ggcgacgcag	tcgatacgag	atcaccttac	ggctggccga	atgagaatga	tccttcgaac	1920
ggacgataca	attggaaatc	ttaccatcca	caagttctcg	taactgatat	gcgatatgag	1980
aatcatggaa	gggaaccgat	gttcaactcaa	cgcaatatgc	atgcgtacac	actctgtgaa	2040
tctacgagga	aggaagggat	tgttgcaa	at	gcagacactc	taacgaagtt	2100
tatattatca	gtcgtggagg	ttacattggc	aaccagcatt	ttggagggaat	gtgggttgga	2160
gacaactctt	cctcccaaag	atacctccaa	atgatgatcg	cgaacatcgt	caacatgaac	2220
atgtcttgcc	ttccactagt	tgggtccgac	attggaggtt	ttacttcgta	tgatggacga	2280
aacgtgtgtc	ccggggatct	aatggtaaga	ttcgtgcagg	cgggttgctt	actaccgtgg	2340
ttcagaaacc	actatggtag	gttggtcgag	ggcaagcaag	agggaaaata	ctatcaagaa	2400
ctgtacatgt	acaaggacga	gatggctaca	ttgagaaaat	tcattgaatt	ccgttaccgc	2460

tggcaggagg tgttgtacac tgctatgtac cagaatgcgg ctttcgggaa accgattatc 2520  
 aaggcagctt ccatgtacga caacgacaga aacgttcgcg gcgcacagga tgaccacttc 2580  
 cttctcggcg gacacgatgg atatcgtatt ttgtgtgcac ctgttgtgtg ggagaataca 2640  
 accagtcgcg atctgtactt gcctgtgctg accaaatggt acaaattcgg ccctgactat 2700  
 gacaccaagc gcctggattc tgcgttggat ggagggcaga tgattaagaa ctattctgtg 2760  
 ccacaaagcg actctccgat atttgtgagg gaaggagcta ttctccctac ccgctacacg 2820  
 ttggacgggt cgaacaagtc aatgaacacg tacacagaca aagacccgtt ggtgtttgag 2880  
 gtattccctc ttggaaacaa ccgtgccgac ggtatgtgtt atcttgatga tggcgggtatt 2940  
 actacagatg ctgaggacca tggcaaattc tctgttatca atgtcgaagc cttacggaaa 3000  
 ggtgttacga cgacgatcaa gtttgcgtat gacacttatt aatacgtatt tgatgggtcca 3060  
 ttctacgttc gaatccgtaa tcttacgact gcatcaaaaa ttaacgtgtc ttctggagcg 3120  
 ggtgaagagg acatgacacc gacctctgcg aactcgaggg cagctttgtt cagtgatgga 3180  
 ggtgttggag aatactgggc tgacaatgat acgtcttctc tgtggatgaa gttgcaaac 3240  
 ctggttctgc aagacgctgt gattaccatt acgtag 3276

<210> 9  
 <211> 3201  
 <212> DNA  
 <213> Unknown

<220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.

<400> 9  
 atggcaggat tttctgatcc tctcaacttt tgcaaagcag aagactacta cagtgttgcg 60  
 ctagactgga agggccctca aaaaatcatt ggagtagaca ctactcctcc aaagagcacc 120  
 aagttcccca aaaactggca tggagtgaac ttgagattcg atgatgggac tttaggtgtg 180  
 gttcagttca ttaggccgtg cgtttggagg gttagatacg accctgggtt caagacctct 240  
 gacgagtatg gtgatgagaa tacgaggaca attgtgcaag attatatgag tactctgagt 300  
 aataaattgg atacttatag aggtccttacg tgggaaacca agtgtgagga ttcgggagat 360  
 ttctttacct tctcatcaa ggtcaccgcc gttgaaaaat ccgagcggac ccgcaacaag 420  
 gtcggcgatg gcctcagaat tcacctatgg aaaagccctt tccgcatcca agtagtgcg 480  
 accttgaccc ctttgaagga tccttacctt attccaaatg tagccgcagc cgaagcccg 540

gtgtccgaca aggtcgtttg gcaaacgtct cccaagacat tcagaaagaa cctgcatccg	600
caacacaaga tgctaaagga tacagttctt gacattgtca aacctggaca tggcgagtat	660
gtggggtggg gagagatggg aggtatccag tttatgaagg agccaacatt catgaactat	720
tttaacttcg acaatatgca ataccagcaa gtctatgccc aaggtgctct cgattctcgc	780
gagccactgt accactcgga tcccttctat cttgatgtga actccaaccc ggagcacaag	840
aatatcacgg caacctttat cgataactac tctcaaattg ccatcgactt tggaaagacc	900
aactcaggct acatcaagct gggaaccagg tatgggtgga tcgattgtta cggatatcagt	960
gcggatacgg tcccggaaat tgtacgactt tatacaggtc ttgttggacg ttcaaagttg	1020
aagcccagat atattctcgg ggcccatcaa gcctgttatg gataccaaca ggaaagtgc	1080
ttgtattctg tgggtccagca gtaccgtgac tgtaaatttc cacttgacgg gattcacgtc	1140
gatgtcgatg ttcaggacgg cttcagaact ttcaccacca acccacacac tttccctaac	1200
cccaaagaga tgtttactaa cttgaggaat aatggaatca agtgctccac caatatcact	1260
cctgttatca gcattaacaa cagagagggg ggatacagta ccctccttga gggagttagc	1320
aaaaaatact ttatcatgga cgacagatat accgagggaa caagtgggaa tgcgaaggat	1380
gttcggtaca tgtactacgg tgggtggaat aaggttgagg tcgatcctaa tgatgttaat	1440
ggtcggccag actttaaaga caactatgac ttccccgcga acttcaacag caaacaatac	1500
ccctatcatg gtggtgtgag ctacggttat gggaacggtg gtgcaggttt ttacccggac	1560
ctcaacagaa aggaggttcg tatctggtgg ggaatgcagt acaagtatct cttcgatatg	1620
ggactggaat ttgtgtggca agacatgact accccagcaa tccacacatc atatggagac	1680
atgaaagggg tgcccacccg tctactcgtc acctcagact ccgtcaccaa tgccctctgag	1740
aaaaagctcg caattgaaac ttgggctctc tactcctaca atctccacaa agcaacttgg	1800
catggtctta gtcgtctcga atctcgtaag aacaaacgaa acttcatcct cgggcgtgga	1860
agttatgccg gagcctatcg ttttgctggt ctctggactg gggataatgc aagtaactgg	1920
gaattctgga agatatcggg ctctcaagtt ctttctctgg gcctcaatgg tgtgtgcatc	1980
gcggggtctg atacgggtgg ttttgaaccc taccgtgatg caaatggggg cgaggagaaa	2040
tactgtagcc cagagctact catcagggtg tatactgggt cattcctctt gccgtggctc	2100
aggaaccatt atgtcaaaaa ggacaggaaa tggttccagg aaccatactc gtaccccaag	2160
catcttgaaa cccatccaga actcgcagac caagcatggc tctataaatc cgttttggag	2220
atctgtaggt actatgtgga gcttagatac tccctcatcc aactacttta cgactgcatg	2280

tttcaaaacg tagtcgacgg tatgccaatc accagatcta tgctcttgac cgatactgag 2340  
 gataccacct tcttcaacga gagccaaaag ttcctcgaca accaatatat ggctggtgac 2400  
 gacattcttg ttgcacccat cctccacagt cgcaaagaaa ttccaggcga aaacagagat 2460  
 gtctatctcc ctctttacca cacctggtac ccctcaaatt tgagaccatg ggacgatcaa 2520  
 ggagtcgctt tggggaatcc tgtcgaaggt ggtagtgtca tcaattatac tgctaggatt 2580  
 gttgcacccg aggattataa tctcttcac agcgtggtac cagtctacgt tagagagggt 2640  
 gccatcatcc cgcaaatcga agtacgccaa tggactggcc agggggggagc caaccgcac 2700  
 aagttcaaca tctaccctgg aaaggataag gagtactgta cctatcttga tgatggtgtt 2760  
 agccgtgata gtgcgccgga agacctcca cagtacaaag agaccacga acagtcgaag 2820  
 gttgaaggcg cgaaaatcgc aaagcagatt ggaaagaaga cgggttaca catctcagga 2880  
 accgaccag aagcaaaggg ttatcacccg aaagttgctg tcacacaaac gtcaaaagac 2940  
 aagacgcgta ctgtcactat tgagccaaaa cacaatggat acgacccttc caaagagggtg 3000  
 ggtgattatt ataccatcat tctttggtac gcaccagggt tcgatggcag catcgtcgat 3060  
 gtgagcaaga cgactgtgaa tgttgagggt ggggtggagc accaagtta taagaactcc 3120  
 gatttacata cggttgttat cgacgtgaag gaggtgatcg gtaccacaaa gagcgtcaag 3180  
 atcacatgta ctgccgctta a 3201

<210> 10  
 <211> 3213  
 <212> DNA  
 <213> Unknown

<220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.

<400> 10  
 atggcaggat tatccgaccc tctcaatttc tgcaaagcag aggactacta cgctgctgcc 60  
 aaaggctgga gtggccctca gaagatcatt cgctatgacc agaccctcc tcagggtaca 120  
 aaagatccga aaagctggca tgcggtaaaac cttcctttcg atgacgggac tatgtgtgta 180  
 gtgcaattcg tcagaccctg tgtttggagg gttagatag accccagtgt caagacttct 240  
 gatgagtacg gcgatgagaa tacgaggact attgtacaag actacatgac tactctggtt 300  
 ggaaacttgg acattttcag aggtcttacg tgggtttcta cgttggagga ttcgggcgag 360  
 tactacacct tcaagtccga agtcactgcc gtggacgaaa ccgaacggac tcgaaacaag 420

gtcggcgacg gcctcaagat ttacctatgg aaaaatccct ttcgcatcca ggtagtgcgt	480
ctcttgaccc ccttgggtga ccccttcccc attcccaacg tagccaatgc cacagcccgt	540
gtggccgaca aggttgtttg gcagacgtcc ccgaagacgt tcaggaaaaa cttgcatccg	600
cagcataaga tgttgaagga tacagttctt gatattatca agccggggca cggagagtat	660
gtgggttggg gagagatggg aggcacgag tttatgaagg agccaacatt catgaattat	720
ttcaactttg acaatatgca atatcagcag gtctatgcac aaggcgctct tgatagtcgt	780
gagccgttgt atcaacttga tcccttctat ctcgacgtga actccaaccc agagcacaag	840
aacattacgg caacctttat cgataactac tctcagattg ccatcgactt tgggaagacc	900
aactcaggct acatcaagct gggtagcagg tatggcggta tcgattgtta cggtatcagc	960
gcggatacgg tcccggagat tgtgcgactt tatactggac ttgttgggcg ttcgaagttg	1020
aagcccagggt atattctcgg agcccaccaa gcttggtatg gataccagca ggaaagtgc	1080
ttgcatgctg ttgttcagca gtaccgtgac accaagtttc cgcttgatgg gttgcatgtc	1140
gatgtcgact ttcaggacaa tttcagaacg tttaccacta acccgattac gttcccta	1200
cccaaagaaa tgtttaccaa tctaaggaac aatggaatca agtgttccac caacatcacc	1260
cctgttatca gtatcagaga tcgcccgaat gggtagagta ccctcaatga gggatatgat	1320
aaaaagtact tcatcatgga tgacagatat accgagggga caagtgggga cccgcaaaat	1380
gttcgatact ctttttacgg cggtgggaac ccggttgagg ttaaccctaa tgatgtttgg	1440
gctcggccag actttggaga caattatgac ttccctacga acttcaactg caaagactac	1500
ccctatcatg gtgggtgtgag ttacggatat gggaaatggca ctccagggtta ctaccctgac	1560
cttaacagag aggaggttcg tatctgggtg ggattgcagt acgagtatct cttcaatatg	1620
ggactagagt ttgtatggca agatatgaca accccagcga tccattcatc atatggagac	1680
atgaaagggg tgcccacccg tctgctcgtc accgccgact cagttaccaa tgctctgag	1740
aaaaagctcg caattgaaag ttgggtctct tactcctaca acctccataa agcaaccttc	1800
cacggtcttg gtcgtcttga gtctcgtaag aacaaacgta acttcatcct cggacgtggg	1860
agttacgccg gtgcctatcg ttttgctggg ctctggactg gagataacgc aagtacgtgg	1920
gaattctgga agatttcggg ctcccaagtt ctttctctag gtctcaatgg tgtgtgtata	1980
gcgggggtctg atacgggtgg ttttgagccc gcacgtactg agattgggga ggagaaatat	2040
tgcagtcocg agctactcat caggtggtat actggatcat tccttttgcc atggcttaga	2100
aaccactacg tcaagaagga caggaaatgg ttccaggaac catacgcgta cccaagcat	2160

cttgaaaccc atccagagct cgcagatcaa gcatggcttt acaaatctgt tctagaaatt 2220  
 tgcagatact gggtagagct aagatattcc ctcatccagc tcctttacga ctgcatgttc 2280  
 caaaacgtgg tcgatgggat gccacttgcc agatctatgc tcttgaccga tactgaggat 2340  
 acgaccttct tcaatgagag ccaaaagtgc ctcgataacc aatatatggc tggtgacgac 2400  
 atccttgtag caccatcct ccacagccgt aacgaggttc cgggagagaa cagagatgtc 2460  
 tatctccctc tattccacac ctggtacccc tcaaacttga gaccgtggga cgatcaggga 2520  
 gtcgctttag ggaatcctgt cgaaggtggc agcggtatca actacactgc caggattgtt 2580  
 gcccagagg attataatct cttccacaac gtggtgccgg tctacatcag agaggggtgc 2640  
 atcattccgc aaattcaggt acgccagtgg attggcgaag gagggcctaa tcccatcaag 2700  
 ttcaatatct accctggaaa ggacaaggag tatgtgacgt accttgatga tgggtgtagc 2760  
 cgcgatagt caccagatga cctcccgag taccgcgagg cctatgagca agcgaaggtc 2820  
 gaaggcaaag acgtccagaa gcaacttgcg gtcattcaag ggaataagac taatgacttc 2880  
 tccgcctccg ggattgataa ggaggcaaag ggttatcacc gcaaagtctc tatcaaacag 2940  
 gagtcaaaaag acaagacccg tactgtcacc attgagccaa aacacaacgg atacgacccc 3000  
 tctaaggaag ttggtaatta ttataccatc attctttggt acgcaccggg ctttgacggc 3060  
 agcatcgctg atgtgagcca ggcgaccgtg aacatcgagg gcgggggtgga atgcgaaatt 3120  
 ttcaagaaca ccggcttgca tacggttgta gtcaacgtga aagaggtgat cggtaccaca 3180  
 aagtccgtca agatcacttg cactaccgct tag 3213

<210> 11  
 <211> 3279  
 <212> DNA  
 <213> Unknown

<220>  
 <223> fungus sp. or fungus infected gracilariopsis sp.

<400> 11  
 atgtttccta ccctgacctt catagcgccc agcgcgctgg ccgccagcac ctttgtgggc 60  
 gcggatatcc gatcgggcat tcgcattcaa tccgctcttc cggccgtgcg caacgctgtg 120  
 cgcaggagca aacattacaa tgtatccatg accgcattgt ctgacaagca aaccgctatc 180  
 agtattggcc ctgacaatcc ggacggtatc aactaccaa actacgatta catccctgta 240  
 gcgggcttta cgccctctc caacaccaac tggatatgctg ccggctcttc cactccgggc 300

ggcatcacgc actggaccgc taccatgaat gtcaaattcg accgcattga caatccgtcg	360
tactccaata accatcctgt tcagattcag gtcacgtcgt acaacaacaa cagcttcagg	420
attcgcttca accctgatgg ccccatcgt gacgtctctc gaggacctat cctgaaacag	480
caactcactt ggattcgaaa ccaggagctg gcgcagggat gtaatccgaa catgagcttc	540
tctcctgaag gttttttgtc ttttgaaacc aaagacctaa acgttataat ctacggcaac	600
tgcaagatga gagtcacgaa gaaggatggc tacctcgtca tggagaatga cgagtgcac	660
tcgcaatcag atggcaataa gtgtagagga ttgatgtacg ttgaccggct atacggtaat	720
gctattgctt ccgtacaaac gaattttcac aaagacactt ctcggaacga gaaattctat	780
ggtgcagggtg aagtcaactg tcgctatgag gagcagggtg aggcgccgac ttatgttcta	840
gaacgctctg gactcgccat gaccaattac aattacgaca acttgaacta caaccaacca	900
gacgtcgttc ctccagggtta tcccgaccat cccaactact acattccaat gtactacgca	960
gcaccgtggt tggtcgttca gggatgcgcg gggacatcga agcaatactc gtacggttgg	1020
tttatggaca atgtctctca gtcgtacatg aacactggag atacggcgtg gaactgcgga	1080
caggaaaacc tggcatacat gggcgcgcaa tacgggccat ttgatcagca ctttgtgtat	1140
ggtgatggag atggccttga agatgtcgtc aaagcgttct cttttcttca aggaaaggag	1200
ttcgaagaca aaaaactcaa caagcgttct gtaatgcctc cgaagtacgt gtttggttct	1260
ttccagggtg ttttcggtgc acttttactg ttgaagcaga atctgcctgc cggagagaac	1320
aacatctcag tgcaagagat tgtggaggggt taccaggata acgactacc ctttgaagg	1380
ctcgcggtag atgttgatat gcaagatgat ctgcgagtgt ttactaccaa accagaatat	1440
tggtcggcaa acatggtagg cgaaggcgggt gatcctaata acagatcagt ctttgaatgg	1500
gcacatgaca ggggccttgt ctgtcagacg aacgtaactt gcttcttgag gaacgataac	1560
agtgggaaac catacgaagt gaatcagaca ttgagggaga aacagttgta tacgaagaat	1620
gattccttga acaacaccga ttttggaact acctcggatg ggcttgga tgctacatt	1680
ggacatttgg actatgggtg tggagtggag tgtgatgcaa tcttcccaga ctggggtcga	1740
ccagacgtgg ctcaatggtg gggagaaaac tacaagaagc tggtcagcat tggctctgat	1800
ttcgtgtggc aggatatgac ggtacctgcg atgatgccgc accgactcgg tgatgctgtc	1860
aacaaaaatt ccggtagtct ggcgccgggc tggccgaatg agaacgatcc atccaacgga	1920
cgatacaact ggaaatctta tcatccgcaa gtgctcgtga ccgacatgcg ctatggtgca	1980
gagtatggaa gggaaccgat ggtgtctcaa cgcaacattc acgcctacac tctttgtgaa	2040

tctaccagac gggaggggaat tgtgggaaac gcagacagtt tgaccaagtt ccgccgcagt 2100  
 tacatcatca gtcgaggagg ttacatcggg aaccagcatt tcggagggat gtgggttggg 2160  
 gacaacagtg ccacagaatc ctacctcaa atgatgttgg cgaacattat caacatgaat 2220  
 atgtcgtgcc tcccgtagt tggctctgat attggcgggt tcaccagta caatgatgcg 2280  
 ggcgacccaa ccccgagga tttgatggta agattcgtgc aggctggctg tctgctaccg 2340  
 tggttcagaa accactatga caggtggatt gagtccaaga agcacgggaa gaaataccag 2400  
 gagttataca tgtaccggg gcaaaaggat acgttgaaga agttcgttga attccgctac 2460  
 cgctggcagg aggttttcta cacagccatg taccaaaatg ctaccactgg agagccgatc 2520  
 atcaaggcgg cgcccatgta caacaacgac gtcaacgtgt ataaatcgca gaatgatcat 2580  
 ttccttctcg gtggacatga cggctatcgt attctctgcg cacctgttgt gcgcgaaaat 2640  
 gcgacaagtc gcgaagtga cctgcctgtg tatagcaagt ggttcaaatt cggaccggac 2700  
 tttgacacta agcccttga aaatgagatt caaggaggtc agacgcttta taattacgct 2760  
 gcaccgctga acgattcgcc gatatttctg agggaaggga ctattcttcc gacacggtac 2820  
 acgctggacg gtgtgaacaa atctatcaac acgtacacag acaatgatcc gcttgtattt 2880  
 gagctgttcc ctctcgaaaa caaccaggcg catggcttgt tctatcatga tgatggcggg 2940  
 gtcaccacca acgctgaaga ctttggcaag tattctgtga tcagtgtgaa ggccgcgcag 3000  
 gaaggttctc aaatgagtgt caagtttgac aatgaagttt atgaacacca atggggagca 3060  
 tcgttctatg ttcgtgttcg taatatgggt gctccgtcta acatcaacgt atcttctcag 3120  
 attggtcaac aggacatgca acagagctcc gtgagttcca gggcgcaa atgttactagt 3180  
 gctaacgatg gcgagtactg ggttgaccag agcacgaact cgttgtggct caagttgcct 3240  
 ggtgcagtta tccaagacgc tgcgatcact gttcgttga 3279

<210> 12  
 <211> 1712  
 <212> DNA  
 <213> Unknown

<220>

<223> fungus sp. or fungus infected gracilariopsis sp.

<400> 12

atgacaaact ataattatga caatttgaac tacaatcaac cggacctcat cccacctggc 60  
 catgattcag atcctgacta ctatattccg atgtactttg cggcaccatg ggtgatcgca 120



catggatata	gtggcaccag	cgaccagtac	tcttatggat	ggtttttgga	caatgtatcc	180
cagtcctaca	caaacactgg	cgatgatgca	tgggctggtc	agaaggattt	ggcgtacatg	240
ggggcacaat	gtgggccttt	cgatcaacat	tttgtgtatg	aggctggaga	tggacttgaa	300
gacgttgtga	ccgcattctc	ttatttgcaa	ggcaaggaat	atgagaacca	gggactgaat	360
atacgttctg	caatgcctcc	gaagtacgtt	ttcggatttt	tccaaggcgt	attcggagcc	420
acatcgctgc	taagggacaa	cttacctgcc	ggcgagaaca	acgtctcttt	ggaagaaatt	480
gttgaaggat	atcaaaatca	gaacgtgcca	tttgaaggtc	ttgctgtgga	tgttgatatg	540
caagatgact	tgagagtgtt	cactacgaga	ccagcgtttt	ggacggcaaa	caaggtgggg	600
gaaggcggtg	atccaaacaa	caagtcagtg	tttgagtggg	cacatgacag	gggccttgtc	660
tgccagacga	atgtaacttg	cttcttgaag	aacgagaaaa	atccttacga	agtgaatcag	720
tcattgaggg	agaagcagtt	gtatacgaag	agtgattcct	tggacaacat	tgattttgga	780
actactccag	atgggcctag	cgatgcgtac	attggacact	tagactacgg	tggtggtgtg	840
gagtgtgatg	cactattccc	agactggggg	cgaccagacg	tggctcaatg	gtggggcgat	900
aactacaaga	aactattcag	cattggtctc	gatttcgtct	ggcaagatat	gacggtacct	960
gcgatgatgc	cgcaccgact	cggtgaccct	gtcggcacia	attccggtga	gacggcgccg	1020
ggctggccga	atgataagga	tccatccaac	ggacgataca	attggaagtc	ttaccatccg	1080
caagtgtctg	tgactgacat	gaggtatgac	gattacggaa	gagatcccat	tgttacgcaa	1140
cgcaatctcc	atgcctacac	tctttgtgag	tctactagga	gggaaggcat	tggtggaaac	1200
gcagatagtc	tgacgaagtt	ccgccgcagc	tatattatca	gtcgtggagg	ctacatcggt	1260
aatcagcact	ttggtgggat	gtgggtagga	gacaactctt	ctacggaaga	ctacctcgca	1320
atgatggtta	tcaacgttat	caacatgaac	atgtccggtg	tcccgtctcg	tggttccgat	1380
attggagggt	tcacggagca	tgacaagaga	aacccttgca	caccggactt	gatgatgaga	1440
tttgtgcagg	ctggatgctt	gctaccgtgg	ttcaggaacc	actacgatag	gtggatcgag	1500
agcaagaaac	acggaaagaa	ctaccaagag	ttgtacatgt	accgcgacca	cttggaacgc	1560
ttgagaagtt	ttgtggaact	ccgctatcgc	tggcaggaag	tggtatacac	agccatgtat	1620
cagaatgctt	tgaacgggaa	gccgatcatc	aaaacggtct	ccatgtacaa	caacgatatg	1680
aacgtcaaag	atgctcagaa	tgaccacttc	ct			1712